

```
|||||
Sbjct 6 TCCTCCGGCCCCTGAATGCG 25
```

> [gi|31790896|gb|AF521554.1|](#) Human coxsackievirus B5 isolate BE00-112 5' UTR, part
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query 1 TCCTCCGGCCCCTGAATGCG 20
        |||||
Sbjct 6 TCCTCCGGCCCCTGAATGCG 25
```

> [gi|31790895|gb|AF521553.1|](#) Human coxsackievirus B5 isolate BE00-45 5' UTR, part:
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query 1 TCCTCCGGCCCCTGAATGCG 20
        |||||
Sbjct 6 TCCTCCGGCCCCTGAATGCG 25
```

> [gi|31790894|gb|AF521552.1|](#) Human echovirus 13 isolate BE00-127 5' UTR, partial s
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query 1 TCCTCCGGCCCCTGAATGCG 20
        |||||
Sbjct 6 TCCTCCGGCCCCTGAATGCG 25
```

> [gi|31790893|gb|AF521551.1|](#) Human echovirus 13 isolate BE00-126 5' UTR, partial s
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query 1 TCCTCCGGCCCCTGAATGCG 20
        |||||
Sbjct 6 TCCTCCGGCCCCTGAATGCG 25
```

> [gi|31790892|gb|AF521550.1|](#) Human echovirus 13 isolate BE00-125 5' UTR, partial s
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```

Query 1 TCCTCCGGCCCCCTGAATGCG 20
      |||||||||||||||||||
Sbjct 6 TCCTCCGGCCCCCTGAATGCG 25

```

> [gi|31790891|gb|AF521549.1](#) Human echovirus 6 isolate BE00-124 5' UTR, partial se
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```

Query 1 TCCTCCGGCCCCCTGAATGCG 20
      |||||||||||||||||||
Sbjct 6 TCCTCCGGCCCCCTGAATGCG 25

```

> [gi|31790890|gb|AF521548.1](#) Human coxsackievirus B5 isolate BE00-123 5' UTR, part
Length=185

Score = 40.1 bits (20), Expect = 0.028
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```

Query 1 TCCTCCGGCCCCCTGAATGCG 20
      |||||||||||||||||||
Sbjct 6 TCCTCCGGCCCCCTGAATGCG 25

```


Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Mar 5, 2006 10:56 PM

Number of letters in database: 427,401,746

Number of sequences in database: 3,774,865

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 3774865

Number of Hits to DB: 132125

Number of extensions: 4781

Number of successful extensions: 4781

Number of sequences better than 1000: 300

Number of HSP's better than 1000 without gapping: 0

Number of HSP's gapped: 4781

Number of HSP's successfully gapped: 306

Length of query: 20

Length of database: 16752467434

Length adjustment: 18

Effective length of query: 2

Effective length of database: 16752467434

Effective search space: 33504934868

Effective search space used: 33369039728

A: 0

X1: 11 (21.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 11 (22.3 bits)

S2: 13 (26.3 bits)

L6 ANSWER 47 OF 49 CAPLUS COPYRIGHT 2006 ACS on STN
 AN 1993:619161 CAPLUS
 DN 119:219161
 TI HIV-1 PCR primers and method of detection using the same
 IN Cassol, Sharon; O'Shaughnessy, Michael; Salas, Teresa; Arella, Max
 PA Can.
 SO Can. Pat. Appl., 60 pp.
 CODEN: CPXXEB
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	-----	----	-----	-----	-----
PI	CA 2039449	AA	19920929	CA 1991-2039449	19910328
PRAI	CA 1991-2039449		19910328		

AB Pathogen nucleic acids on a supported sample are detected by amplification and detection of the amplified nucleic acids. Detection of HIV-1 by PCR using inosine-substituted "consensus" primers based on known primers SK68 and SK69 was demonstrated. The modified primers are highly specific and sensitive and they prevent false neg. results due to variation in the HIV-1 genome. These PCR primers were used to detect HIV-1 nucleic acid in dried blood spots collected on filter paper. The blood was extracted from the filter paper and phenol/CHCl3 was added. A tRNA carrier was added to the treated extract, and the nucleic acids were precipitated with NH4OAc prior to the PCR amplification/detection procedure. The method of the invention gave fewer false-neg. results than the standard PCR performed on mononuclear cell lysates, and the results were highly concordant with serol. evidence of HIV infection.

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3079	(sscp or single adj1 strand adj1 conformation) same (PCR or polymerase adj1 chain)	US-PGPUB; USPAT	OR	ON	2006/03/07 07:09
L2	66	l1 same (virus or viral)	US-PGPUB; USPAT	OR	ON	2006/03/07 07:11
L3	3	"9743420"	EPO; DERWENT	OR	ON	2006/03/07 07:11

=> d his full

(FILE 'HOME' ENTERED AT 06:28:22 ON 07 MAR 2006)

FILE 'MEDLINE, CAPLUS' ENTERED AT 06:28:36 ON 07 MAR 2006

L1 2287 SEA (PANVIRUS OR UNIVERSAL) (3A) PRIMER#
L2 61 SEA L1 (9A) (VIRUS OR VIRAL)
L3 48 DUP REM L2 (13 DUPLICATES REMOVED)
L4 0 SEA PANVIRAL (3A) PRIMER#
L5 48 DUP REM L3 (0 DUPLICATES REMOVED)
D 1-48 TI
D 33, 36, 38, 43, 44, 46 48 BIB AB

FILE 'STNGUIDE' ENTERED AT 06:32:00 ON 07 MAR 2006

FILE 'MEDLINE, CAPLUS' ENTERED AT 06:34:56 ON 07 MAR 2006
D 12, 20, 23 BIB AB

FILE 'STNGUIDE' ENTERED AT 06:34:56 ON 07 MAR 2006

FILE 'MEDLINE, CAPLUS' ENTERED AT 06:35:56 ON 07 MAR 2006

L6 51525 SEA CONSERV? (9A) (SEQUENCE OR PRIMER#)
L7 65677 SEA CONSERV? (9A) (SEQUENCE# OR PRIMER#)
L8 9547 SEA L7 AND (VIRUS? OR VIRAL?)
L9 47 SEA L8 AND (MASS (3A) SPECTRO? OR MALDI)
L10 39 DUP REM L9 (8 DUPLICATES REMOVED)
D 1-39 TI
D 30 BIB AB
L11 386 SEA L8 AND ELECTROPHOR?
L12 297 DUP REM L11 (89 DUPLICATES REMOVED)
L13 226 SEA L12 AND PY<2001
D 1-226 TI
L14 85 SEA L13 AND (PCR OR POLYMERASE (W) CHAIN)
D 1-85 TI
D 50 85 BIB AB
D 23 BIB AB

FILE 'STNGUIDE' ENTERED AT 06:47:28 ON 07 MAR 2006

FILE 'MEDLINE, CAPLUS' ENTERED AT 06:54:03 ON 07 MAR 2006
D 13, 41, 51 37 BIB AB

FILE 'STNGUIDE' ENTERED AT 06:54:04 ON 07 MAR 2006

FILE 'MEDLINE, CAPLUS' ENTERED AT 06:56:49 ON 07 MAR 2006

L15 520 SEA (SSCP) AND (PCR OR POLYMERASE (W) CHAIN) AND (VIRUS? OR
VIRAL?)
L16 324 SEA L15 AND PY<2001
L17 244 DUP REM L16 (80 DUPLICATES REMOVED)
L18 0 SEA L17 AND (UNIVERSAL OR INOSINE)
D L17 1-244 TI
L19 57 SEA L17 AND (CONSERV? OR VARIAB? OR HYPERVARIA?)
D 1-57 TI
D L17 157 210 BIB AB

FILE 'STNGUIDE' ENTERED AT 07:05:15 ON 07 MAR 2006

FILE HOME

FILE MEDLINE

FILE LAST UPDATED: 4 MAR 2006 (20060304/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).

See also:

<http://www.nlm.nih.gov/mesh/>
http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE CAPLUS

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FILE COVERS 1907 - 7 Mar 2006 VOL 144 ISS 11
FILE LAST UPDATED: 6 Mar 2006 (20060306/ED)

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FILE STNGUIDE
FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Mar 3, 2006 (20060303/UP).

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